

SEQUENCE LISTING

<110> TANABE SEIYAKU CO., LTD.

<120> A Novel Phospholipase A₂ and the gene thereof.

<130> 03-004-PCT

<150> JP2002-008435

<151> 2002-01-17

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<170> PatentIn Ver. 2.0

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<223> Artificially synthesized primer sequence

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<400> 2

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<213> Homo sapiens

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 Met Glu Ser Leu Ser Pro
 1 5
 ggg gga cca act ggc cac cct tac cag ggg gag gcc tct acc tgc tgg 164
 Gly Gly Pro Thr Gly His Pro Tyr Gln Gly Glu Ala Ser Thr Cys Trp
 10 15 20
 cag ctc aca gtg agg gtc ctg gag gcg cgg aac ctg cgc tgg gct gac 212
 Gln Leu Thr Val Arg Val Leu Glu Ala Arg Asn Leu Arg Trp Ala Asp
 25 30 35
 ctg ttg agt gag gcc gac cct tac gtg atc cta cag ctg tgc acc gca 260
 Leu Leu Ser Glu Ala Asp Pro Tyr Val Ile Leu Gln Leu Ser Thr Ala
 40 45 50
 cct gga atg aag ttt aag acc aag acg ctc acc gac acc agt cat cct 308
 Pro Gly Met Lys Phe Lys Thr Lys Thr Leu Thr Asp Thr Ser His Pro
 55 60 65 70
 gtg tgg aat gag gcc ttc cgt ttc ctt atc caa agt cag gtc aag aat 356
 Val Trp Asn Glu Ala Phe Arg Phe Leu Ile Gln Ser Gln Val Lys Asn
 75 80 85
 gtt ctg gag ctt agc atc tat gat gag gac tca gtc acg gag gat gac 404
 Val Leu Glu Leu Ser Ile Tyr Asp Glu Asp Ser Val Thr Glu Asp Asp
 90 95 100
 atc tgc ttc aag gtt ctc tat gac atc tca gaa gtc ctc cct ggc aag 452
 Ile Cys Phe Lys Val Leu Tyr Asp Ile Ser Glu Val Leu Pro Gly Lys
 105 110 115
 ctg ctc cgg aaa acc ttc tcc cag agt ccc cag gga gag gag gag ctg 500
 Leu Leu Arg Lys Thr Phe Ser Gln Ser Pro Gln Gly Glu Glu Glu Leu
 120 125 130

gat gtg gag ttc ctg atg gaa gaa acg tca gat cgc cca gaa aac ctc	548
Asp Val Glu Phe Leu Met Glu Glu Thr Ser Asp Arg Pro Glu Asn Leu	
135 140 145 150	
atc acc aac aaa gtc att gtg gcc cga gag ctg tca tgc ctg gat gtg	596
Ile Thr Asn Lys Val Ile Val Ala Arg Glu Leu Ser Cys Leu Asp Val	
155 160 165	
cat ctg gac agc aca ggg agc acc gct gtg gtt gca gat cag gac aag	644
His Leu Asp Ser Thr Gly Ser Thr Ala Val Val Ala Asp Gln Asp Lys	
170 175 180	
ctg gag ctg gag ctg gtg ctg aag ggg tcc tat gag gac aca cag aca	692
Leu Glu Leu Glu Leu Val Leu Lys Gly Ser Tyr Glu Asp Thr Gln Thr	
185 190 195	
tcc ttc ctg ggc aca gcc tct gcc ttc cgc ttc cac tac atg gca gcc	740
Ser Phe Leu Gly Thr Ala Ser Ala Phe Arg Phe His Tyr Met Ala Ala	
200 205 210	
cia gag aca gag ctg agc ggg cgc ctg agg agc tcc aga agc aat ggc	788
Leu Glu Thr Glu Leu Ser Gly Arg Leu Arg Ser Ser Arg Ser Asn Gly	
215 220 225 230	
tgg aat ggg gac aac tca gct ggg tac ctc act gtg ccc ctg agg ccc	836
Trp Asn Gly Asp Asn Ser Ala Gly Tyr Leu Thr Val Pro Leu Arg Pro	
235 240 245	
tig acc att ggg aag gag gtg act atg gat gtt cct gct cca aat gcc	884
Leu Thr Ile Gly Lys Glu Val Thr Met Asp Val Pro Ala Pro Asn Ala	
250 255 260	
cca gga gtg agg ctg cag ctc aag gca gag ggc tgc cct gag gag ctg	932
Pro Gly Val Arg Leu Gln Leu Lys Ala Glu Gly Cys Pro Glu Glu Leu	
265 270 275	
gcc gtg cac ctg ggc ttc aat ctc tgt gca gag gag cag gcc ttc ctg	980
Ala Val His Leu Gly Phe Asn Leu Cys Ala Glu Glu Gln Ala Phe Leu	
280 285 290	
agc agg agg aag cag gtg gtg gcc aag gcc ctg aag cag gcc ctg cag	1028
Ser Arg Arg Lys Gln Val Val Ala Lys Ala Leu Lys Gln Ala Leu Gln	
295 300 305 310	
ctg gac aga gac ctg cag gag gat gag gta ccc gtt gtg ggc atc atg	1076
Leu Asp Arg Asp Leu Gln Glu Asp Glu Val Pro Val Val Gly Ile Met	
315 320 325	
gcc aca gga gga ggt gcc cgg gcc atg acc tca ctc tac ggc cac cta	1124

Ala Thr Gly Gly Gly Ala Arg Ala Met Thr Ser Leu Tyr Gly His Leu	
330 335 340	
ttg gcc ttg cag aag ctg ggc ctc cta gac tgt gtg acc tac ttc agt	1172
Leu Ala Leu Gln Lys Leu Gly Leu Leu Asp Cys Val Thr Tyr Phe Ser	
345 350 355	
ggc atc tct ggc tct acg tgg aca atg gcc cac ctg tac ggg gac cct	1220
Gly Ile Ser Gly Ser Thr Trp Thr Met Ala His Leu Tyr Gly Asp Pro	
360 365 370	
gag tgg tct cag agg gac ctg gag gga cct atc aga tac gcc cgg gag	1268
Glu Trp Ser Gln Arg Asp Leu Glu Gly Pro Ile Arg Tyr Ala Arg Glu	
375 380 385 390	
cac ctg gcc aag agc aag ctg gag gtc ttt tcc cca gag cgc ctg gcg	1316
His Leu Ala Lys Ser Lys Leu Glu Val Phe Ser Pro Glu Arg Leu Ala	
395 400 405	
agc tac cgc cgg gag ctg gag ctg cgg gct gag cag ggc cac ccc acg	1364
Ser Tyr Arg Arg Glu Leu Glu Leu Arg Ala Glu Gln Gly His Pro Thr	
410 415 420	
acc ttt gtg gac ctg tgg gcg cta gtc ctg gag tcc atg ctg cac ggc	1412
Thr Phe Val Asp Leu Trp Ala Leu Val Leu Glu Ser Met Leu His Gly	
425 430 435	
cag gtg atg gat cag aag ctg tca gga cag aga gcc gcc ctg gaa cgg	1460
Gln Val Met Asp Gln Lys Leu Ser Gly Gln Arg Ala Ala Leu Glu Arg	
440 445 450	
ggt cag aac cct ctg ccc ctc tac ttg agc ctc aat gtc aaa gag aac	1508
Gly Gln Asn Pro Leu Pro Leu Tyr Leu Ser Leu Asn Val Lys Glu Asn	
455 460 465 470	
aat ctg gag aca ctg gac ttc aag gag tgg gtt gag ttc tcc ccc tat	1556
Asn Leu Glu Thr Leu Asp Phe Lys Glu Trp Val Glu Phe Ser Pro Tyr	
475 480 485	
gag gtc ggt ttc ctg aag tac ggg gcc ttc gtc cct cct gag ctc ttc	1604
Glu Val Gly Phe Leu Lys Tyr Gly Ala Phe Val Pro Pro Glu Leu Phe	
490 495 500	
ggc tcc gag ttc ttc atg gga cgg ctg atg agg agg atc ccg gag ccc	1652
Gly Ser Glu Phe Phe Met Gly Arg Leu Met Arg Arg Ile Pro Glu Pro	
505 510 515	
cgg atc tgc ttt ctg gaa gcc atc tgg agc aac att ttc tcc ctg aac	1700
Arg Ile Cys Phe Leu Glu Ala Ile Trp Ser Asn Ile Phe Ser Leu Asn	

520	525	530	
ctg ctg gat gcc tgg tat gac ctc acc agt tct ggg gag tcc tgg aaa			1748
Leu Leu Asp Ala Trp Tyr Asp Leu Thr Ser Ser Gly Glu Ser Trp Lys			
535	540	545	550
cag cac atc aag gac aag acc agg agc tta gag aag gag ccc ctg acc			1796
Gln His Ile Lys Asp Lys Thr Arg Ser Leu Glu Lys Glu Pro Leu Thr			
	555	560	565
acc tcg ggg acc tcc tcg cgg ctg gag gcc tcg tgg ctg cag cca ggc			1844
Thr Ser Gly Thr Ser Ser Arg Leu Glu Ala Ser Trp Leu Gln Pro Gly			
	570	575	580
acg gcg ctg gcc cag gca ttt aaa ggc ttc ctg aca ggc agg ccc ctc			1892
Thr Ala Leu Ala Gln Ala Phe Lys Gly Phe Leu Thr Gly Arg Pro Leu			
	585	590	595
cac cag cgc agc ccc aac ttc ctc cag ggc ctc cag ctg cac cag gac			1940
His Gln Arg Ser Pro Asn Phe Leu Gln Gly Leu Gln Leu His Gln Asp			
	600	605	610
tac tgt agc cac aaa gac ttc tcc acc tgg gca gac tac cag ctt gac			1988
Tyr Cys Ser His Lys Asp Phe Ser Thr Trp Ala Asp Tyr Gln Leu Asp			
615	620	625	630
tcc atg ccc agc cag ctg acc ccc aag gag ccc cgg ctc tgc ctg gtg			2036
Ser Met Pro Ser Gln Leu Thr Pro Lys Glu Pro Arg Leu Cys Leu Val			
	635	640	645
gac gcc gcc tac ttc atc aac acc agc tct ccc tcc atg ttc cgg cca			2084
Asp Ala Ala Tyr Phe Ile Asn Thr Ser Ser Pro Ser Met Phe Arg Pro			
	650	655	660
ggc cgc agg ctg gac ctc atc ctc tcc ttc gac tac tcc cta tct gcg			2132
Gly Arg Arg Leu Asp Leu Ile Leu Ser Phe Asp Tyr Ser Leu Ser Ala			
	665	670	675
ccc ttc gag gca ctg cag cag acg gag ctg tac tgc cgg gcc cgg ggg			2180
Pro Phe Glu Ala Leu Gln Gln Thr Glu Leu Tyr Cys Arg Ala Arg Gly			
	680	685	690
ctg ccc ttc ccc cgg glg gaa ccc agc cct cag gac cag cac cag cca			2228
Leu Pro Phe Pro Arg Val Glu Pro Ser Pro Gln Asp Gln His Gln Pro			
695	700	705	710
agg gaa tgc cac ctc ttc tca gac ccc gcc tgc ccc gag gcc ccg atc			2276
Arg Glu Cys His Leu Phe Ser Asp Pro Ala Cys Pro Glu Ala Pro Ile			
	715	720	725

ctg ctg cac ttc ccg ctg gtc aat gcc tcc ttc aag gac cac tca gcc	2324
Leu Leu His Phe Pro Leu Val Asn Ala Ser Phe Lys Asp His Ser Ala	
730 735 740	
ccc ggt gtc cag cgc agc ccc gca gag ctg cag ggt ggc caa gtg gat	2372
Pro Gly Val Gln Arg Ser Pro Ala Glu Leu Gln Gly Gly Gln Val Asp	
745 750 755	
ctc acc ggg gcc acc tgc ccc tac acc ctg tcc aac atg acc tac aag	2420
Leu Thr Gly Ala Thr Cys Pro Tyr Thr Leu Ser Asn Met Thr Tyr Lys	
760 765 770	
gag gaa gac ttc gag cgc ctg ctg cgg ctg agt gac tac aac gtg cag	2468
Glu Glu Asp Phe Glu Arg Leu Leu Arg Leu Ser Asp Tyr Asn Val Gln	
775 780 785 790	
acc agc cag ggt gcc atc ctg cag gcc ctg agg acc gcg ctg aag cac	2516
Thr Ser Gln Gly Ala Ile Leu Gln Ala Leu Arg Thr Ala Leu Lys His	
795 800 805	
cgg act cta gag gcg agg cct cca agg gca cag acc tgaggttgct	2562
Arg Thr Leu Glu Ala Arg Pro Pro Arg Ala Gln Thr	
810 815	
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cttagaattt tctgtagaca gatcatgcca tctccaaata gagatgggtt tacttcttcc	3282

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 atgta 3587

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 Asn Leu Arg Trp Ala Asp Leu Leu Ser Glu Ala Asp Pro Tyr Val Ile
 35 40 45
 Leu Gln Leu Ser Thr Ala Pro Gly Met Lys Phe Lys Thr Lys Thr Leu
 50 55 60
 Thr Asp Thr Ser His Pro Val Trp Asn Glu Ala Phe Arg Phe Leu Ile
 65 70 75 80
 Gln Ser Gln Val Lys Asn Val Leu Glu Leu Ser Ile Tyr Asp Glu Asp
 85 90 95
 Ser Val Thr Glu Asp Asp Ile Cys Phe Lys Val Leu Tyr Asp Ile Ser
 100 105 110
 Glu Val Leu Pro Gly Lys Leu Leu Arg Lys Thr Phe Ser Gln Ser Pro
 115 120 125
 Gln Gly Glu Glu Glu Leu Asp Val Glu Phe Leu Met Glu Glu Thr Ser
 130 135 140
 Asp Arg Pro Glu Asn Leu Ile Thr Asn Lys Val Ile Val Ala Arg Glu
 145 150 155 160

Leu Ser Cys Leu Asp Val His Leu Asp Ser Thr Gly Ser Thr Ala Val
 165 170 175
 Val Ala Asp Gln Asp Lys Leu Glu Leu Glu Leu Val Leu Lys Gly Ser
 180 185 190
 Tyr Glu Asp Thr Gln Thr Ser Phe Leu Gly Thr Ala Ser Ala Phe Arg
 195 200 205
 Phe His Tyr Met Ala Ala Leu Glu Thr Glu Leu Ser Gly Arg Leu Arg
 210 215 220
 Ser Ser Arg Ser Asn Gly Trp Asn Gly Asp Asn Ser Ala Gly Tyr Leu
 225 230 235 240
 Thr Val Pro Leu Arg Pro Leu Thr Ile Gly Lys Glu Val Thr Met Asp
 245 250 255
 Val Pro Ala Pro Asn Ala Pro Gly Val Arg Leu Gln Leu Lys Ala Glu
 260 265 270
 Gly Cys Pro Glu Glu Leu Ala Val His Leu Gly Phe Asn Leu Cys Ala
 275 280 285
 Glu Glu Gln Ala Phe Leu Ser Arg Arg Lys Gln Val Val Ala Lys Ala
 290 295 300
 Leu Lys Gln Ala Leu Gln Leu Asp Arg Asp Leu Gln Glu Asp Glu Val
 305 310 315 320
 Pro Val Val Gly Ile Met Ala Thr Gly Gly Gly Ala Arg Ala Met Thr
 325 330 335
 Ser Leu Tyr Gly His Leu Leu Ala Leu Gln Lys Leu Gly Leu Leu Asp
 340 345 350
 Cys Val Thr Tyr Phe Ser Gly Ile Ser Gly Ser Thr Trp Thr Met Ala
 355 360 365
 His Leu Tyr Gly Asp Pro Glu Trp Ser Gln Arg Asp Leu Glu Gly Pro
 370 375 380
 Ile Arg Tyr Ala Arg Glu His Leu Ala Lys Ser Lys Leu Glu Val Phe
 385 390 395 400
 Ser Pro Glu Arg Leu Ala Ser Tyr Arg Arg Glu Leu Glu Leu Arg Ala
 405 410 415
 Glu Gln Gly His Pro Thr Thr Phe Val Asp Leu Trp Ala Leu Val Leu

420	425	430
Glu Ser Met Leu His Gly Gln Val Met Asp Gln Lys Leu Ser Gly Gln		
435	440	445
Arg Ala Ala Leu Glu Arg Gly Gln Asn Pro Leu Pro Leu Tyr Leu Ser		
450	455	460
Leu Asn Val Lys Glu Asn Asn Leu Glu Thr Leu Asp Phe Lys Glu Trp		
465	470	475
Val Glu Phe Ser Pro Tyr Glu Val Gly Phe Leu Lys Tyr Gly Ala Phe		
485	490	495
Val Pro Pro Glu Leu Phe Gly Ser Glu Phe Phe Met Gly Arg Leu Met		
500	505	510
Arg Arg Ile Pro Glu Pro Arg Ile Cys Phe Leu Glu Ala Ile Trp Ser		
515	520	525
Asn Ile Phe Ser Leu Asn Leu Leu Asp Ala Trp Tyr Asp Leu Thr Ser		
530	535	540
Ser Gly Glu Ser Trp Lys Gln His Ile Lys Asp Lys Thr Arg Ser Leu		
545	550	555
Glu Lys Glu Pro Leu Thr Thr Ser Gly Thr Ser Ser Arg Leu Glu Ala		
565	570	575
Ser Trp Leu Gln Pro Gly Thr Ala Leu Ala Gln Ala Phe Lys Gly Phe		
580	585	590
Leu Thr Gly Arg Pro Leu His Gln Arg Ser Pro Asn Phe Leu Gln Gly		
595	600	605
Leu Gln Leu His Gln Asp Tyr Cys Ser His Lys Asp Phe Ser Thr Trp		
610	615	620
Ala Asp Tyr Gln Leu Asp Ser Met Pro Ser Gln Leu Thr Pro Lys Glu		
625	630	635
Pro Arg Leu Cys Leu Val Asp Ala Ala Tyr Phe Ile Asn Thr Ser Ser		
645	650	655
Pro Ser Met Phe Arg Pro Gly Arg Arg Leu Asp Leu Ile Leu Ser Phe		
660	665	670
Asp Tyr Ser Leu Ser Ala Pro Phe Glu Ala Leu Gln Gln Thr Glu Leu		
675	680	685

Tyr Cys Arg Ala Arg Gly Leu Pro Phe Pro Arg Val Glu Pro Ser Pro
690 695 700

Gln Asp Gln His Gln Pro Arg Glu Cys His Leu Phe Ser Asp Pro Ala
705 710 715 720

Cys Pro Glu Ala Pro Ile Leu Leu His Phe Pro Leu Val Asn Ala Ser
725 730 735

Phe Lys Asp His Ser Ala Pro Gly Val Gln Arg Ser Pro Ala Glu Leu
740 745 750

Gln Gly Gly Gln Val Asp Leu Thr Gly Ala Thr Cys Pro Tyr Thr Leu
755 760 765

Ser Asn Met Thr Tyr Lys Glu Glu Asp Phe Glu Arg Leu Leu Arg Leu
770 775 780

Ser Asp Tyr Asn Val Gln Thr Ser Gln Gly Ala Ile Leu Gln Ala Leu
785 790 795 800

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805 810 815

Gln Thr

<210> 10

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially synthesized primer sequence

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<211> 30

<212> DNA

<213> Artificial Sequence

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<223> Artificially synthesized primer sequence

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